



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/931,375

Source: OIPE

Date Processed by STIC: 08/23/2001

RECEIVED

FEB 14 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/931,375

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)          contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)    Sequence(s)          missing. If intentional, please insert the following lines for each skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>    Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 06/04/2001

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE



## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,375

DATE: 08/23/2001

TIME: 17:07:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

3 <110> APPLICANT: WARMAN, Matthew L.  
 4 GONG, Yaoqin  
 5 OLSEN, Bjorn R.  
 6 RAWADI, Georges  
 7 ROMAN-ROMAN, Sergio  
 8  
 9 <120> TITLE OF INVENTION: REGULATOR GENE AND SYSTEM USEFUL FOR THE DIAGNOSIS AND  
 THERAPY OF

Does Not Comply  
 Corrected Diskette Needed

See page 6 of 8A

10 OSTEOPOROSIS  
 12 <130> FILE REFERENCE: 38464-0004  
 14 <140> CURRENT APPLICATION NUMBER: US/09/931,375  
 14 <141> CURRENT FILING DATE: 2001-08-17

14 <150> PRIOR APPLICATION NUMBER: US 60/304,851  
 15 <151> PRIOR FILING DATE: 2001-07-13  
 17 <150> PRIOR APPLICATION NUMBER: US 60/234,337  
 18 <151> PRIOR FILING DATE: 2000-09-22  
 20 <150> PRIOR APPLICATION NUMBER: US 60/226,119  
 21 <151> PRIOR FILING DATE: 2000-08-18

23 <160> NUMBER OF SEQ ID NOS: 89  
 25 <170> SOFTWARE: PatentIn version 3.0

27 <210> SEQ ID NO: 1

28 <211> LENGTH: 5063

29 <212> TYPE: DNA

30 <213> ORGANISM: Homo sapiens

32 <400> SEQUENCE: 1

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39	cggctgggtg	acgccggcgg	agtcaggctg	gagtcaccca	tcgtggtcag	cggcctggag	240
41	gatgcggccg	cagtggactt	ccagttttcc	aagggagccg	tgtactggac	agacgtgagc	300
43	gaggaggcca	tcaagcagac	ctacctgaac	cagacggggg	ccgccgtgca	gaacgtggtc	360
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47	tggacggact	cagagaccaa	ccgcacgcag	gtggccaacc	tcaatggcac	atcccgaag	480
49	gtgctcttct	ggcaggacct	tgaccagcct	agggccatcg	ccttggaccc	cgctcacggg	540
51	tacatgtact	ggacagactg	gggtgagacg	ccccggattg	agcgggcagg	gatggatggc	600
53	agcaccggga	agatcattgt	ggactcggac	atttactggc	ccaatggact	gaccatcgac	660
55	ctggaggagc	agaagctcta	ctgggctgac	gccaagctca	gcttcatcca	ccgtgccaac	720
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67	cccacgggtg	tgcagctgca	ggacaacggc	aggacgtgta	aggcaggagc	cgaggagggtg	1080
69	ctgctgctgg	cccggcgggac	ggacctacgg	aggatctcgc	tggacacgcc	ggacttcacc	1140
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77	gactgggtgg	cccgaacct	ctactggacc	gacacgggca	cggaccgcat	cgagggtgacg	1380
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TIME: 17:07:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

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89	aagctcccg	acattttcgg	gttcacgctg	ctgggggact	tcatctactg	gactgactgg	1740
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93	cagctgcccg	acctgatggg	gctcaaagct	gtgaatgtgg	ccaaggtcgt	cggaaccaac	1860
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129	cccaccacct	tcttgctgtt	cagccagaaa	tctgccatca	gtcggatgat	cccggacgac	2940
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133	tatgaccac	tggacaagtt	catctactgg	gtggatgggc	gccagaacat	caagcgagcc	3060
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165	ccctgcgcgc	gggttcagtg	tgtggacctg	cgctgagcgt	gcgacggcga	ggcagactgt	4020
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PATENT APPLICATION: US/09/931,375

DATE: 08/23/2001  
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Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

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215 20 25 30
217 Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala
218 35 40 45
220 Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp
221 50 55 60
223 Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr
224 65 70 75 80
226 Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly
227 85 90 95
229 Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
230 100 105 110
232 Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
233 115 120 125
235 Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val
236 130 135 140
238 Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala Leu Asp Pro
239 145 150 155 160
241 Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile
242 165 170 175
244 Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser
245 180 185 190
247 Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
248 195 200 205
250 Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
251 210 215 220
253 Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro
254 225 230 235 240
256 Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
257 245 250 255

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TIME: 17:07:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

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260          260          265          270
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263          275          280          285
265 Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu Asp Asn Gly
266          290          295          300
268 Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro Phe Tyr Thr
269 305          310          315          320
271 Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly Arg Thr Cys
272          325          330          335
274 Lys Ala Gly Ala Glu Glu Val Leu Leu Ala Arg Arg Thr Asp Leu
275          340          345          350
277 Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile Val Leu Gln
278          355          360          365
280 Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu
281          370          375          380
283 Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile Arg Arg Ala
284 385          390          395          400
286 Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn
287          405          410          415
289 Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn Leu Tyr Trp
290          420          425          430
292 Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu Asn Gly Thr
293          435          440          445
295 Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile
296          450          455          460
298 Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp Trp Gly Glu
299 465          470          475          480
301 Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu Arg Arg Val
302          485          490          495
304 Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala Leu Asp Leu
305          500          505          510
307 Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu
308          515          520          525
310 Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys
311          530          535          540
313 Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe Ile Tyr Trp
314 545          550          555          560
316 Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala
317          565          570          575
319 Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys
320          580          585          590
322 Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys Ala Asp Arg
323          595          600          605
325 Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His Ala Thr Arg
326          610          615          620
328 Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met Lys Thr Cys
329 625          630          635          640
331 Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala Ala Ile His

```

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338          675          680          685
340 Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg Ala Phe Met
341          690          695          700
343 Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu Asp Tyr Pro
344 705          710          715          720
346 Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr Trp Ala Asp
347          725          730          735
349 Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg
350          740          745          750
352 Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser Leu Ala Leu
353          755          760          765
355 Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly Gly Lys Pro
356          770          775          780
358 Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met Thr Leu Val
359 785          790          795          800
361 Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr Ala Asp Gln
362          805          810          815
364 Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu Ser Ser Asn
365          820          825          830
367 Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu Pro His Pro
368          835          840          845
370 Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr Asp Trp Asn
371          850          855          860
373 Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg Asn Arg Thr
374 865          870          875          880
376 Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His
377          885          890          895
379 Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn Asn Gly Gln
380          900          905          910
382 Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys
383          915          920          925
385 Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro
386          930          935          940
388 Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser Arg Met Ile
389 945          950          955          960
391 Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu His Gly Leu
392          965          970          975
394 Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys Phe Ile Tyr
395          980          985          990
397 Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr
398          995          1000          1005
400 Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn Pro Asp
401          1010          1015          1020
403 Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu
404          1025          1030          1035

```

Errored 09/931,375

210> 3  
211> 20  
212> DNA  
213> Artificial Sequence

400> 3  
gctgccct agacttagcc 20

210> 4  
211> 18  
212> DNA  
213> Artificial Sequence

400> 4  
caagtcgct tccgagac 18

210> 5  
211> 20  
212> DNA  
213> Artificial Sequence

400> 5

(When the 213 response is  
"Artificial Sequence" a  
mandatory response is required  
in field 223.

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/931,375

DATE: 08/23/2001

TIME: 17:07:13

Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:528 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:528 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:537 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:537 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:546 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:546 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:555 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:555 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:564 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:564 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:573 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:573 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:582 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:582 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:591 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:591 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:600 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:600 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:609 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:609 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:618 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:618 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:627 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:627 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:636 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:636 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:645 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:645 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:654 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:654 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:663 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:663 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:672 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:672 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:681 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:681 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:690 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:690 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:699 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:708 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:708 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:717 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:717 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:726 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:726 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/931,375

DATE: 08/23/2001

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Input Set : A:\ES.txt

Output Set: N:\CRF3\08162001\I931375.raw

L:735 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:735 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:744 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:744 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:787 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32 ✓  
L:862 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40